

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: May 19, 2003, 16:43:18 ; Search time 29.0436 Seconds
(without alignments)
1237.942 Million cell updates/sec

Title: US-09-625-573-2
Perfect score: 1970
Sequence: 1 MLSTSRFRINTNESGEEV.....GKKSIGRAPEASLQDKEGA 374

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1970	100.0	374	2 I38450	chemokine (C-C) re
2	1651.5	83.8	360	2 JC2443	chemokine (C-C) re
3	1224	62.1	352	2 A43113	chemokine (C-C) re
4	967.5	49.1	355	2 A45177	chemokine (C-C) re
5	960	48.7	359	2 I49341	MIP-1 alpha recept
6	902.5	45.8	355	2 I49339	macrophage inflam
7	890.5	45.2	355	2 G02436	chemokine (C-C) re
8	833	42.3	360	2 JC4587	chemokine (C-C) re
9	831.5	42.2	360	2 A57160	chemokine (C-C) re
10	794.5	40.3	383	2 S55594	G protein-coupled
11	731	37.1	356	2 I49340	MIP-1 alpha recept
12	723	36.7	355	2 JC5067	G protein-coupled
13	704.5	35.8	354	2 I58186	probable G protein-
14	698	35.4	355	2 JC4304	orphan G protein-c
15	644.5	32.7	344	2 JC5942	chemokine receptor
16	584	29.6	378	2 B55735	lymphocyte-specifi
17	575.5	29.2	378	2 A55735	G protein-coupled
18	570	28.9	378	2 A45680	G protein-coupled
19	554.5	28.1	369	2 JC5068	G protein-coupled
20	541.5	27.5	360	2 A53611	interleukin-8 rece
21	537	27.3	359	2 A48921	interleukin-8 rece
22	531	27.0	352	2 G00048	fusin (LESTRA) - c
23	530.5	26.9	353	2 S28787	neuropeptide Y/pep
24	529.5	26.9	355	2 JQ1231	interleukin-8 rece
25	528	26.8	352	2 A54747	neuropeptide Y/pep
26	526	26.7	358	2 A53752	interleukin-8 rece
27	526	26.7	367	2 JE0349	interferon-inducib
28	524.5	26.6	350	2 A39445	interleukin-8 rece
29	523	26.5	356	2 S42096	interleukin-8 rece

RESULT 1

I38450

Chemokine (C-C) receptor 2, splice form A - human

N/Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte

C/Species: Homo sapiens (man)

C/Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999

C/Accession: I38450

R/Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.

Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994

A/Title: Molecular cloning and functional expression of two monocyte chemoattractant

A/Reference number: A53477; MUID:94195821; PMID:8146186

A/Accession: I38450

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-374 <RES>

A/Cross-references: EMBL:U03882; NID:g472555; PIDN:AAA19119.1; PID:g472556

C/Genetics:

A/Gene: GDB:CMKBR2

A/Cross-references: GDB:337364; OMIM:601267

A/Map position: 3p21-3p21

C/Superfamily: vertebrate rhodopsin

C/Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmem

F;44-68/Domain: transmembrane #status predicted <TM1>

F;79-95/Domain: transmembrane #status predicted <TM2>

F;115-136/Domain: transmembrane #status predicted <TM3>

F;154-178/Domain: transmembrane #status predicted <TM4>

F;208-226/Domain: transmembrane #status predicted <TM5>

F;244-265/Domain: transmembrane #status predicted <TM6>

F;292-309/Domain: transmembrane #status predicted <TM7>

F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;32-277,113-190/Disulfide bonds: #status predicted

Query Match 100.0%; Score 1970; DB 2; Length 374;

Best Local Similarity 100.0%; Pred. No. 2.8e-167;

Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRFRINTNESGEEVTFDFDYDGAPCHFDVKVQIGAQLLPPLYSLVFIFGFYGN 60

DB 1 MLSTSRFRINTNESGEEVTFDFDYDGAPCHFDVKVQIGAQLLPPLYSLVFIFGFYGN 60

QY 61 MLVLLILINCKKLCLETDIYLLNLATSDLLFLITLPLWAHSAANEWFGNAMCKLFTGLY 120

DB 61 MLVLLILINCKKLCLETDIYLLNLATSDLLFLITLPLWAHSAANEWFGNAMCKLFTGLY 120

QY 121 HIGYFGGIFILLITIDRYLAIVHAVFALKARTVTEGVVTSVITWLVAFAVSVPGLIIFTK 180

DB 121 HIGYFGGIFILLITIDRYLAIVHAVFALKARTVTEGVVTSVITWLVAFAVSVPGLIIFTK 180

QY 181 CQKEDSVVCGPYFPRGNNEFTIMRNILGLVLPILLIMVICYSGILTKLLRCRNEKKRHR 240

DB 181 CQKEDSVVCGPYFPRGNNEFTIMRNILGLVLPILLIMVICYSGILTKLLRCRNEKKRHR 240

30 519 26.3 333 2 I65989 G protein-coupled
31 484 24.6 350 2 JN0621 G protein-coupled
32 480 24.4 359 2 A42656 angiotensin II rec
33 479.5 24.3 374 2 S42628 G protein-coupled
34 475 24.1 359 2 I51372 angiotensin II rec
35 473 24.0 359 2 JC2134 angiotensin II rec
36 472 24.0 359 2 JQ1516 angiotensin II rec
37 471 23.9 359 2 S15403 angiotensin II rec
38 471 23.9 359 2 S15403 angiotensin II rec
39 469 23.8 359 2 JC1104 angiotensin II rec
40 468 23.8 359 2 S44425 angiotensin II rec
41 465 23.6 359 2 JC1194 angiotensin II rec
42 465 23.6 374 2 S32785 angiotensin II rec
43 464 23.6 359 2 A48857 angiotensin II rec
44 461.5 23.4 372 2 S26667 G protein-coupled
45 460.5 23.4 327 2 S56162 MDCR15 protein - h

ALIGNMENTS

QY 241 AVRVIPTIMIVYFLFWTPYNIIVILLNTFOEFGLSNCESTSQLODQATQVTEITLGMTHCCI 300
 Db 241 AVRVIPTIMIVYFLFWTPYNIIVILLNTFOEFGLSNCESTSQLODQATQVTEITLGMTHCCI 300
 QY 301 NPIIYAVGKFRSLFHIALGCRITAPLQKPVCGGPGVPGKRVKVTTOGLLDGRGKXSI 360
 Db 301 NPIIYAVGKFRSLFHIALGCRITAPLQKPVCGGPGVPGKRVKVTTOGLLDGRGKXSI 360
 QY 361 GRAPEASLODKEGA 374
 Db 361 GRAPEASLODKEGA 374
 RESULT 2
 JC2443
 Chemokine (C-C) receptor 2, splice form B - human
 N:Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
 C:Species: Homo sapiens (man)
 C:Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
 A:Accession: JC2443; 138463
 A:Title: Molecular cloning and functional expression of a human monocyte chemoattractant prot
 A:Reference number: JC2443; MUID:94324942; PMID:8048929
 A:Molecule type: mRNA
 A:Residues: 1-360 <YAM>
 A:CROSS-references: DDBJ:D29984; NID:g531246; PIDN:BAA06253.1; PID:g531247
 R:Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
 A:Title: Molecular cloning and functional expression of two monocyte chemoattractant pro
 A:Reference number: A53477; MUID:94195821; PMID:8146186
 A:Accession: 138463
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-360 <RES>
 A:CROSS-references: EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PID:g472558
 C:Genetics:
 A:Gene: GDB:CMKBR2
 A:CROSS-references: GDB:337364; OMIM:601267
 A:Map position: 3p21-3p21
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: alternate splicing; G protein-coupled receptor; glycoprotein; transmembran
 F:81-100/Domain: transmembrane #status predicted <TM2>
 F:115-136/Domain: transmembrane #status predicted <TM3>
 F:154-178/Domain: transmembrane #status predicted <TM4>
 F:207-226/Domain: transmembrane #status predicted <TM5>
 F:244-268/Domain: transmembrane #status predicted <TM6>
 F:287-309/Domain: transmembrane #status predicted <TM7>
 F:14/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:113-190/Disulfide bonds: #status predicted
 Query Match 83.8%; Score 1651.5; DB 2; Length 360;
 Best Local Similarity 95.5%; Pred. No. 5.3e-139;
 Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;
 QY 1 MLSTSRSPRINTNSGSEVTFDDYDYGAPCHKFDVKQIGAGQLLPPLSLVFIFFGVGN 60
 Db 1 MLSTSRSPRINTNSGSEVTFDDYDYGAPCHKFDVKQIGAGQLLPPLSLVFIFFGVGN 60
 QY 61 MLVVLILNCKKLCLTDIYLLNLALISDLFLITPLWAHSAANWVFGNAMCKLFTGLY 120
 Db 61 MLVVLILNCKKLCLTDIYLLNLALISDLFLITPLWAHSAANWVFGNAMCKLFTGLY 120
 QY 121 HIGYEGGIFFIILLIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
 Db 121 HIGYEGGIFFIILLIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
 QY 181 COKEDSVVCGPFFPRGNWTFIMRNILGLVLPILIMVICYSGILKTLRLCRNEKKRHR 240
 Db 181 COKEDSVVCGPFFPRGNWTFIMRNILGLVLPILIMVICYSGILKTLRLCRNEKKRHR 240

QY 241 AVRVIPTIMIVYFLFWTPYNIIVILLNTFOEFGLSNCESTSQLODQATQVTEITLGMTHCCI 300
 Db 241 AVRVIPTIMIVYFLFWTPYNIIVILLNTFOEFGLSNCESTSQLODQATQVTEITLGMTHCCI 300
 QY 301 NPIIYAVGKFRSLFHIALGCRITAPLQKPVCGGPGVPGKRVKVTTOGLLDGRGKXSI 327
 Db 301 NPIIYAVGKFRSLFHIALGCRITAPLQKPVCGGPGVPGKRVKVTTOGLLDGRGKXSI 334

RESULT 3

A43113

Chemokine (C-C) receptor 5 - human

N:Alternate names: C-C CKR-5; CCR5

C:Species: Homo sapiens (man)

C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000

A:Accession: A43113; S71808; A58834; A58832; G02653; A58833

R:Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.

Biochemistry 35, 3362-3367, 1996

A:Title: Molecular cloning and functional expression of a new human CC-chemokine rec

A:Reference number: A43113; MUID:96241590; PMID:8639485

A:Accession: A43113

A:Molecule type: mRNA

A:Residues: 1-352 <SAMI>

A:CROSS-references: GB:X91492; NID:gl262810; PIDN:CAA62796.1; PID:gl262811

R:Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Sarrac

M.; Imail, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.;

Nature 382, 722-725, 1996

A:Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant allele

A:Reference number: S71808; MUID:96345670; PMID:8751444

A:Accession: S71808

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 182-206; 207-230 <SAM2>

A:Accession: A58834

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-184, 'IKDHLGAGPAAACHGHLGNPKNSASVSK' <SAM3>

A:CROSS-references: GB:X99393; NID:gl524062; PIDN:CAA67767.1; PID:gl524063

A:Note: This frameshift mutation results in a non-functional receptor but confers a

nd may have had a selective advantage by conferring resistance to Yersinia plague inf

R:Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.

J. Leukoc. Biol. 60, 147-152, 1996

A:Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine

A:Reference number: A58832; MUID:96295970; PMID:8699119

A:Accession: A58832

A:Molecule type: mRNA

A:Residues: 1-352 <COM1>

A:CROSS-references: GB:U57840; NID:gl502408; PIDN:AAB17071.1; PID:gl502409

A:Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes

R:Combadiere, C.

submitted to the EMBL Data Library, May 1996

A:Reference number: H01541

A:Accession: G02653

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-89, 'L', 91-352 <COM2>

A:CROSS-references: EMBL:U57840

R:Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.

J. Biol. Chem. 271, 17161-17166, 1996

A:Title: Molecular cloning and functional characterization of a novel human CC chemok

A:Reference number: A58833; MUID:96291862; PMID:8663314

A:Accession: A58833

A:Molecule type: mRNA

A:Residues: 1-352 <RAP>

A:CROSS-references: GB:U54994; NID:gl457945; PIDN:AAC50598.1; PID:gl457946

C:Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (

C:Genetics:

A:Gene: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CKR5; ChemR13

A:CROSS-references: GDB:1230510; OMIM:601373

A:Map position: 3p21-3p21

A:Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RA

A;Note: probably acts to control granulocyte proliferation and differentiation
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane
 F;32-56/Domain: transmembrane #status predicted <TM1>
 F;67-87/Domain: transmembrane #status predicted <TM2>
 F;103-124/Domain: transmembrane #status predicted <TM3>
 F;142-166/Domain: transmembrane #status predicted <TM4>
 F;193-218/Domain: transmembrane #status predicted <TM5>
 F;236-257/Domain: transmembrane #status predicted <TM6>
 F;285-300/Domain: transmembrane #status predicted <TM7>
 F;20-269,101-178/Disulfide bonds: #status predicted
 F;268/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
 F;340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 62.1%; Score 1224; DB 2; Length 352;
 Best Local Similarity 76.3%; Pred. No. 4.8e-101;
 Matches 235; Conservative 27; Mismatches 34; Indels 12; Gaps 3;

QY 24 FDYDY--GAPCHKFDVKQIGAGQALLPPLYSLVFIFGFGNMLVVLINCKKLCITDIYL 81
 Db 10 YDINYTSEPCQINKVQIARLLPPLYSLVFIFGFGNMLVVLINCKKLSMTDIYL 69

QY 82 LNLASDLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGFIITLIDRYLA 141
 Db 70 LNLASDLFLITLPLVPEWAHSAANEWFGNAMCKLFTGLYHIGYFGGFIITLIDRYLA 129

QY 142 IVHAVFALKARTVFGVTSVITLWVAFAVPGIIFTKCKEDSVVCGPYPP---RG 197
 Db 130 VHAVFALKARTVFGVTSVITLWVAFAVPGIIFTKCKEDSVVCGPYPP---RG 189

QY 198 WNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKRRHRAVRVIFIMIVYFLWT 257
 Db 190 WKNFQILKIVILGLVPLLMVICYSGILKTLRCRNEKRRHRAVRVIFIMIVYFLWA 249

QY 258 PYNIVLLNTFQEFFGLSNCESTSQLDOATQVTTGLMTHCCINPIIYAFVGEKFSLF- 316
 Db 250 PYNIVLLNTFQEFFGLSNCESTSQLDOATQVTTGLMTHCCINPIIYAFVGEKFSLF 309

QY 317 -----HTA 319
 Db 310 VFFQKHIA 317

RESULT 4
 A45177
 Chemokine (C-C) receptor 1 - human
 N;Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
 C;Accession: A45177; I55671
 R;Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
 Cell 72, 415-425, 1993
 A;Title: Molecular cloning, functional expression, and signaling characteristics of a C-
 A;Reference number: A45177; MUID:93161416; PMID:7679328
 A;Accession: A45177
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-355 <NEO>
 A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
 A;Experimental source: HL60 cells
 A;Note: sequence extracted from NCBI backbone (NCBIP:124876)
 R;Gao, J.
 J. Exp. Med. 177, 1421-1427, 1993
 A;Title: Structure and functional expression of the human macrophage inflammatory 1 alpha
 A;Reference number: I55671; MUID:93240122; PMID:7693036
 A;Accession: I55671
 A;Status: preliminary;
 A;Molecule type: mRNA
 A;Residues: 1-355 <RES>
 A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
 A;Genetics:
 A;Gene: GDB:CMKBR1; CMKR-1

A;Cross-references: GDB:138446; OMIM:601159
 A;Map position: 3p21-3p21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein
 F;36-60/Domain: transmembrane #status predicted <TM1>
 F;71-91/Domain: transmembrane #status predicted <TM2>
 F;108-129/Domain: transmembrane #status predicted <TM3>
 F;147-171/Domain: transmembrane #status predicted <TM4>
 F;205-223/Domain: transmembrane #status predicted <TM5>
 F;240-264/Domain: transmembrane #status predicted <TM6>
 F;288-305/Domain: transmembrane #status predicted <TM7>
 F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;24-273,106-183/Disulfide bonds: #status predicted
 F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 49.1%; Score 967.5; DB 2; Length 355;
 Best Local Similarity 58.7%; Pred. No. 2.9e-78;
 Matches 185; Conservative 47; Mismatches 72; Indels 11; Gaps 5;

QY 12 NTNSESGETVTFDYDYGAPCHKFDVKQIGAGQALLPPLYSLVFIFGFGNMLVVLINCK 71
 Db 5 NTTED-YDTTFEFDYGATPCQKYNRAFGAQLPPLYSLVFIFGFGNMLVVLVQYK 63

QY 72 KLKCLTDIYLLNLALISDLLFLITLPLWA-HSAANEWFGNAMCKLFTGLYHIGYFGGIF 130
 Db 64 RLKNNTSIYLLNLALISDLLFLITLPLFPWIDYKLDKDDWFGDAMCKILSGFYTYGLYSEIF 123

QY 131 IILLTIDRYLAIVHAVFALKARTVFGVTSVITLWVAFAVPGIIFTKCKEDSVVVC 190
 Db 124 IILLTIDRYLAIVHAVFALKARTVFGVTSVITLWVAFAVPGIIFTKCKEDSVVVC 183

QY 191 GPYPP----RGWNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKRRHRAVRVIF 246
 Db 184 SLHPHESLRBWKLFQALKNLGLVPLLMVICYSGILKTLRCRNEKRRHRAVRVIF 242

QY 247 TIMIVFLFWTPYNNIVLLNTFQEFFGLSNCESTSQLDOATQVTTGLMTHCCINPIYA 306
 Db 243 VIMIIFFLWTPYNNIVLLNTFQEFFGLSNCESTSQLDOATQVTTGLMTHCCINPIYA 302

QY 307 FVGEKF----RSLFH 317
 Db 303 FVGERFRKYLQQLFH 317

RESULT 5
 I49341
 MIP-1 alpha receptor like-2 - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998
 C;Accession: I49341
 R;Gao, J.L.; Murphy, P.M.
 J. Biol. Chem. 270, 17494-17501, 1995
 A;Title: Cloning and differential tissue-specific expression of three mouse beta chain
 A;Reference number: I49341
 A;Accession: I49341
 A;Status: preliminary;
 A;Molecule type: DNA
 A;Residues: 1-359 <RES>
 A;Cross-references: EMBL:U28406; NID:g881551; PID:g881552
 C;Superfamily: vertebrate rhodopsin

Query Match 48.7%; Score 960; DB 2; Length 359;
 Best Local Similarity 50.1%; Pred. No. 1.4e-77;
 Matches 187; Conservative 59; Mismatches 89; Indels 38; Gaps 7;

QY 10 IRNTNESGEVTFDYDYGAPCHKFDVKQIGAGQALLPPLYSLVFIFGFGNMLVVLIN 69
 Db 8 IKTVESEF--TTPYEWEAPPCEKVRKEIGSLWLLPPLYSLVFIFGFGNMLVVLILIK 65

QY 70 CKKLKCLTDIYLLNLALISDLLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGI 128
 Db 66 YRKLQIMTNIYLLNLALISDLLFLITLPLWVAFAVPGIIFTKCKEDSVVVC 125

QY 129 FFILLITIDRYLAIVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVY 188
Db 126 FFILLITIDRYLAIVHAFALRARTVTFATITSIITWGLAGLALPEFIPHESQDSFCE 185
QY 189 VCGPYEPFG---WNNFHTIMRNILGLVPLLLIMVICYSGLIKTLRCRNEKKHRAVRV 244
Db 186 SCSPPYEGEEDSWKRFHARMMIFGLALPPLVVMVICYSGLIKTLRCRNEKKHRAIRL 244
QY 245 IFTIMIVYFLWTPYINIVILLNTFQEFFGLSNCESTSQLDQATQVETLGMTHCCINPII 304
Db 245 IFWVMIVFTFWTPYINLVLLFSAFHSTFLETSCEQSKHLDLAWQVTEVIATHCVCNPI 304
QY 305 YAFVGEKFRS---LFHIALGCRIALPQKPVCGPGVGRKNNKVVTTQGL---LDGRGK 357
Db 305 YAFVGERFRKRLFFH-----RNVQFTWENIFQFLPGEENG 341
QY 358 KSIGRAPEASLOD 370
Db 342 RTSSVSPSTGEQE 354

RESULT 6
I49339
macrophage inflammatory protein-1 alpha receptor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C:Accession: I49339
R:Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokines
A:Reference number: I49339; MUID:95340546; PMID:7542241
A:Accession: I49339
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-355 <RES>
A:Cross-references: EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548
C:Superfamily: vertebrate rhodopsin

Query Match 45.8%; Score 902.5; DB 2; Length 355;
Best Local Similarity 53.1%; Pred. No. 1.7e-72;
Matches 170; Conservative 58; Mismatches 75; Indels 17; Gaps 6;
QY 21 TTFDYDYGAPCHKFDVQKIGAQLLPPLYSLVFIFGVGNMLVLLINCKLKCLTDIY 80
Db 13 TTFDYDGTSPCKQAVRAFAGLLPPLYSLVFIFGVGNMLVLLINCKLKCLTDIY 72
QY 81 LNLAISSDLLFLITPLWA-HSAANEWFGNACKLFTGLYHIGYFGGIFFIILLTDIY 139
Db 73 LNLAVSLLVFLTPFWIDYKLDKDWIFGDAMCKLLSGFYGLYSEIFFIILLTDIY 132
QY 140 LAIVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFP--- 195
Db 133 LAIVHAFALRARTVTLGITSITWALAILASMPALYFFKAQWETHTRCSPHFYKSL 192
QY 196 RGNWFHTIMRNILGLVPLLLIMVICYSGLIKTLRCRNEKKHRAVRVFTIMIVYFLF 255
Db 193 KQMKRFQALKNLGLLGLPPLVLMVICYAGIIRILLR-RESEKVKAVRLIFATLLEFLL 251
QY 256 WTPYINIVILLNTFQEFFGLSNCESTSQLDQATQVETLGMTHCCINPIIYAFVGEKFR--- 312
Db 252 WTPYINLSVFSAFQDVLFTNQCEQSKHLDLAWQVTEVIATHCVCNPIIYVFGVERFWKY 311
QY 313 -RSLF--HIALGCRIALPQK 329
Db 312 LRQFQHVAVI-----PLAK 326

RESULT 7
G02436
chemokine (C-C) receptor 3 - human
N:Alternate names: C-C CR-3
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000

C:Accession: G02436; A57237
R:Ponath, P.D.
submitted to the EMBL Data Library, February 1996
A:Reference number: H01272
A:Accession: G02436
A>Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-355 <PON>
A:Cross-references: EMBL:U49727; NID:g1477560; PIDN:AAB09726.1; PID:g1477561
R:Combiadere, C.; Ahuja, S.K.; Murphy, P.M.
J. Biol. Chem. 270, 16491-16494, 1995
A:Title: Cloning and functional expression of a human eosinophil CC chemokine receptor
A:Reference number: A57237; MUID:95348056; PMID:7622448
A:Accession: A57237
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-106, N', 108-275, S', 277-280, R', 282-355 <COM>
A:Cross-references: GB:U28694; NID:g1199579; PIDN:AAC50469.1; PID:g1199580
A:Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC5040401 is incorrect
C:Genetics:
A:Gene: GDB:CMKBR3
A:Cross-references: GDB:579624; OMIM:601268
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane F; 36-60/Domain: transmembrane #status predicted <TM1>
F:71-91/Domain: transmembrane #status predicted <TM2>
F:108-129/Domain: transmembrane #status predicted <TM3>
F:147-171/Domain: transmembrane #status predicted <TM4>
F:205-223/Domain: transmembrane #status predicted <TM5>
F:240-261/Domain: transmembrane #status predicted <TM6>
F:288-305/Domain: transmembrane #status predicted <TM7>
F:24-273, 106-183/Disulfide bonds: #status predicted
F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 45.2%; Score 890.5; DB 2; Length 355;
Best Local Similarity 54.6%; Pred. No. 2e-71;
Matches 167; Conservative 56; Mismatches 72; Indels 11; Gaps 5;
QY 21 TTFDYDYGAPCHKFDVQKIGAQLLPPLYSLVFIFGVGNMLVLLINCKLKCLTDIY 80
Db 14 TSYVD-DVGLLCEKADTRALMAQFVPLYSLVFVGLLGNVVMILIKYRRIRMTNIY 72
QY 81 LNLAISSDLLFLITPLWAHSA-ANEWFGNACKLFTGLYHIGYFGGIFFIILLTDIY 139
Db 73 LNLAISSDLLFLITPLFWTHYVRGHNWVFGHGMCKLLSGFYGLYSEIFFIILLTDIY 132
QY 140 LAIVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFP--- 196
Db 133 LAIVHAFALRARTVTFGVITSITWGLAVLALPEFIFETEELFEELTCLSAIYEDTV 192
QY 197 -GWNFHTIMRNILGLVPLLLIMVICYSGLIKTLRCRNEKKHRAVRVFTIMIVYFLF 255
Db 193 YSRHFHTLRMTFICLVPLVMAICYTGIIKTLRCPS-KKKYKAIRLIFIVMAVFFIF 251
QY 256 WTPYINIVILLNTFQEFFGLSNCESTSQLDQATQVETLGMTHCCINPIIYAFVGEKFRS- 314
Db 252 WTPYINLSVFSAFQDVLFTNQCEQSKHLDLAWQVTEVIATHCVCNPIIYAFVGERFKY 311
QY 315 ---LFH 317
Db 312 LRHEFH 317

RESULT 8
JC4587
chemokine (C-C) receptor 4 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C:Accession: JC4587
R:Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A:Title: Molecular cloning of murine CC CR-4 and high affinity binding of chemokines

A:Reference number: JC4587; MUID:96136324; PMID:8573157
A:Accession: JC4587
A:Molecule type: mRNA
A:Residues: 1-360 <HOO>
A:Cross-references: EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167852
A:Experimental source: thymus
C:Genetics:
A:Gene: cc ckr-4
C:Superfamily: vertebrate rhodopsin
C:Keywords: glycoprotein; phosphoprotein; receptor; thymus
F:2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:72,202,350/Binding site: phosphate (Ser) (covalent) (by protein kinase II) #status predicted
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 42.3%; Score 833; DB 2; Length 360;
Best Local Similarity 47.9%; Pred. No. 2.6e-66;
Matches 160; Conservative 63; Mismatches 89; Indels 22; Gaps 5;

QY 10 IRTNNEGEVTFDYD-YGAPCHKFDVKQIGCAQLLPPLYSLVIFGFGVGNMVLVILI 68
DB 6 VTDITQDETIVNSYFYFESMPKPCKEGAKFGEVLPPLYSLVIFLGLFGNSVVLVLF 65

QY 69 NCKKLCITDIYLLALSDILFLITPLWAHSAANEVFGNAMCKLFTGLYHIGYFGGI 128
DB 66 KYKRLKMTDVLNLAISDLLFLVSLPWPWYAADQWVGLGCKIVSWMYLVGFYSGI 125

QY 129 FFIILLTIDRYLAIVHAFVAVFASVPGIIFTCOKEDSVY 188
DB 126 FFIIMLSIDRYLAIVHAFVAVFASVPGIIFTCOKEDSVY 185

QY 189 VCGPYF---PRGNFHTIMRNILGLPLLMVICYSIGILKTLRCRNEKRRHRAVVI 245
DB 186 YCKTQISVNSTWTKVLSLEINVLGLLPLGLMFWYSMIITLQCKNEKK-NRAVRMI 244

QY 246 FTIMIVYFLFPYNYVILLNTFOEFGLSNCESTSQLDAQVTTGLMTHCCINPIIY 305
DB 245 FGWVVLFGFWPYNVFLFLEVLQDCTLERYDYAIOATETLGLFIHCCINPVIY 304

QY 306 AVFGKFR-----SLPHIALGCRAPLOKPVCGGP 335
DB 305 FFLGKFRKIYQLFR-----TCRGP 325

RESULT 9
A57160
chemokine (C-C) receptor 4 - human
N:Alternate names: C-C CKR-4
P:Species: Homo sapiens (man)
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C:Accession: A57160
R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogwerf, A.J.; Proudfoot, A.E.I.; W
J. Biol. Chem. 270, 19495-19500, 1995
A:Title: Molecular cloning and functional expression of a novel CC chemokine receptor cl
A:Reference number: A57160; MUID:95370289; PMID:7642634
A:Accession: A57160
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-360 <POW>
A:Cross-references: GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452
A:Note: source clone K5-5
C:Genetics:
A:Gene: GDB:CMKBR4
A:Cross-references: GDB:677463
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F:40-65/Domain: transmembrane #status predicted <TM1>
F:76-97/Domain: transmembrane #status predicted <TM2>
F:112-133/Domain: transmembrane #status predicted <TM3>
F:151-175/Domain: transmembrane #status predicted <TM4>
F:208-226/Domain: transmembrane #status predicted <TM5>
F:243-264/Domain: transmembrane #status predicted <TM6>

F:291-308/Domain: transmembrane #status predicted <TM7>
F:29-276,110-187/disulfide bonds: #status predicted
F:72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 42.2%; Score 831.5; DB 2; Length 360;
Best Local Similarity 51.9%; Pred. No. 3.5e-66;
Matches 154; Conservative 58; Mismatches 80; Indels 5; Gaps 3;

QY 31 PCKHEDVKQIGCAQLLPPLYSLVIFGFGVGNMVLVILINCKKLCITDIYLLMATSDDL 90
DB 28 PCKEGIKAFGELEFPPLYSLVIFGFGVGNMVLVILINCKKLCITDIYLLMATSDDL 87

QY 91 FLITPLWAHSAANEVFGNAMCKLFTGLYHIGYFGGIIFILLTIDRYLAIVHAFVAVF 150
DB 88 FVFLPFPWGYAADQWVGLGCKIMSWYLVGFYSGIFVFMLSIDRYLAIVHAFVAVF 147

QY 151 ARTVTFGVVTSVITWLVAVFASVPGIIFTCOKEDSVYVCGPYFPRG---WNNFHTIMRN 207
DB 148 ARTLYGVITSLATWSVAVFASVPGIIFTCOKEDSVYVCGPYFPRG---WNNFHTIMRN 207

QY 208 ILGLVPLLMVICYSIGILKTLRCRNEKRRHRAVVIITMIVYFLFPTPYNIVILLNT 267
DB 208 ILGLVPLLMVICYSIGILKTLRCRNEKRRHRAVVIITMIVYFLFPTPYNIVILLNT 266

QY 268 FOEFGLSNCESTSQLDAQVTTGLMTHCCINPIIYAFVGEKFRS-LPHIALGCR 323
DB 267 LVELEVLQDCTPFRYLDYAIQATETLAFVHCCCLNPPIIYFELGKFRKIYQLFQTCR 323

RESULT 10
RS5594
G protein-coupled receptor E1 - equine herpesvirus 2
C:Species: equine herpesvirus 2
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
C:Accession: RS5594
R:Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A:Title: The DNA sequence of equine herpesvirus 2.
A:Reference number: RS5594; MUID:95302501; PMID:7783207
A:Accession: RS5594
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-383 <TEL>
A:Cross-references: GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 40.3%; Score 794.5; DB 2; Length 383;
Best Local Similarity 44.3%; Pred. No. 7.2e-63;
Matches 164; Conservative 60; Mismatches 107; Indels 39; Gaps 7;

QY 4 TSSRFRTRNNEGEVTFDYD---GAPCHKFDVKQIGCAQLLPPLYSLVIFGFGVGNM 61
DB 32 TTIASLVPTSNSSDYDDLDVDEBAPCYKSDTTLAAQVVPALYLVFLFGLGNI 91

QY 62 LVVLILNCKKLCITDIYLLNLAISDLLFLITPLWAH---SAANEVFGNAMCKLFTGL 119
DB 92 LVVIIVRYWKIRKINMLNLAISDLLFLITPLFWMHYIGMVDWTFGLSCKLLRGV 151

QY 120 YHIGYFGGIIFILLTIDRYLAIVHAFVAVFASVPGIIFTCOKEDSVYVCGPYF 179
DB 152 CYMSLYSQVECIILLTIDRYLAIVHAFVAVFASVPGIIFTCOKEDSVYVCGPYF 211

QY 180 KOKEDSVYVCGPYF---RGWNNFHTIMRNILGLVPLLMVICYSIGILKTLRCRNE 235
DB 212 GHODDNGRVQCDPYYPPEMSTNVWRRHAKVIMLSLILPLIMAVCYVIITRLLR-RPS 270

QY 236 KKRHRAVVIITMIVYFLFPTPYNIVILLNTFOEFGLSNCESTSQLDAQVTTGLM 295
DB 271 KKYKAIKRLIFVIMVAVFVFWTPYNIIVILLSTFHTATLLNLOCAUSNLMALLTKTVAY 330

G protein-coupled receptor **CKR-11** - human
 JC5067
 Alternate names: chemokine receptor-like protein **TER1**; **GPR-CY6**
 C.Species: *Homo sapiens* (man)
 C.Date: 31-Jan-1997 sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
 C.Revision: G02776; G02776; G02387
 C.Accession: JC5067; G02776; G02387
 R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
 R:Rizaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
 A:Title: Molecular cloning and RNA expression of two new human chemokine re
 A:Reference number: JC5067; MUID:97040707; PMID:8886020
 A:Accession: JC5067
 A:Reference number: JC5067
 A:Molecule type: DNA
 A:Residues: 1-355 <ZAB>
 A.Cross-references: EMBL:Z79782; MID:g1668735; PIDN:CAB02142.1; PID:g166873
 R:Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Sa
 submitted to the EMBL Data Library, June 1996
 A:Reference number: H01714
 A:Accession: G02776
 A:Status: translated from **GB/EMBL/DBDJ**
 A:Molecule type: DNA

Query Match 35.8%; Score 704.5; DB 2; Length 354;

